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FIG. 1

atgttagccaacagctcctcaaccAACAGTTCTCCCGTGTCCGTACTACCGACCT
 acccaccgcctgcacttggtggtcacAGCTTGGTGTGGCTGCCGGCTCCCCCTCAAC
 gcgctagccctctgggtttcctgcgcgcgtgcgcgtgcacTCGGTGGTAGCGTGTAC
 atgtgtAACCTGGCGGCCAGCAGACTGCTTCAACCTCTCGCTGCCGTTGTCTCC
 tactacgcactgcaccactggccctccccgacccctgtGCCAGACAGACGGCGCCATC
 ttccagatgaacatgtacggcagctgcacTCCCTGTGCGACCTGCACCGTGGACCGCTAC
 gcccacatcgacccgcgtgcacTGCGCCACCTGCACCGTGGCGCCCGTGGCGCGCTG
 ctctgcctggcgtgtggcgctcatcctggtgtttGCCGTGCCGCGCCGCGTGCAC
 aggccctcgcttgcgcgtaccggacctcgaggcgccatgcggatcggatcggatc
 gagcggatgtggaaaggcaggctgcgcctcgatgcgtgtggccgaggcgctggcttc
 ctgc
 cccgacGCCACGCCAGAGCGAGCGGGCGGGAGACCGTGCACCGTGCACCGTGCAC
 gtcatctcctgtgtgcgcctacaacAGCACGCGCTGGCGGTCTACGGCTGCTG
 CGGAGCAAGCTGGTGGCGCCAGCGTGCCTGCACCGTGCACCGTGCACCGTGCAC
 GTGATGGTGTGCTGGCGCGCCAACCTGCACCGTGCACCGTGCACCGTGCAC
 GCCGAGGGCTCCGCAACACCCCTGCACCGTGCACCGTGCACCGTGCACCGTGCAC
 GCCACCAACGGGACGCACCGTGCACCGTGCACCGTGCACCGTGCACCGTGCAC
 GCCACCAAGGCCGGATGCCGCCAGTCAGGGCTGCTCCGACCCCTCCGACTCCCAC
 TCTCCTCACACAGTGTCCCCAGGATTCCGCCCTCTGA

FIG. 2

MLANSSTNSSVLPDPYRPTHRLHLVVYSLVLAAGLPLNALALWVFLRALRVHSVSVY
 MCNLAASDLLFTLSLPVRLSYYALHHWPFPDLLCQTTGAIIFQMNMYGSCIFLMLINVDRY
 AAIHVPLRLRHLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVRLCFESFS
 DELWKGRLLPLVILLAECALGFLLPLAAVYSSGRFWTLARPDATQSQRRLKTVRLLLNL
 VIFLLCFVPYNSTLAVYGLLRSKLVAASVPARDRVRGVLMVMVLLAGANCVLDPYVYFS
 AEGFRNTLRGLGTPHRARTSATNGTRAALAQSERSAVTTDATRPDAASQGLLRPSDSHSL
 SSFTQCPQDSAL

FIG. 3A

gcgtccgaaaaaaaaaaaaattccttacataactacaacatgaatagatcttggaaacat
tatgctaagtgaaaataaaccagacacaaaaggacaatattgttatgattccactcatatg
aggtatctagaataggcaaattcattgagacagaaaagttagactagaaccagaagctgaat
gggtgcggtagtactgcttaatgactgcagagttgtgcttggatgatgaaaaag
ttctattctggaaacagagactgtgacggtaagcaacactgtcttggatgatgatgatgatg
tggtgttgtgtttgagacggactctcactctgtctccaggccggagtgcgatggat
tagacctgctaggggagcacattggcaaaactcaacccacagggcctccctgcctagca
agactgtgtcaatttattcacatgtggcttggatgactagcatgcaatcagcc
tatgagggcattattatattatcccatttacagatgaagaaactgagaagtcaaa
ccattaagctgaacccagttgcttgcaccacaaatccagccctcacaggcgactgt
catgtatgcgtaaggctggatgttgcattttgttgcattttgttgcattttgc
ttgtctgacatggagtctcactctgtcaccaggctggatgcagtgccgtatctcg
tcactgcaacccgcctccgggttcaaggacttcctgcagcctccatgtactc
aaagagttgaccatttattcttgataatgaggagctagcctagcacctggatccaagg
gtgctccataagaccacattgattgttgcatttatctgtctccctcaatggatg
taaaggaggtggggcaaaagacttttgcattttgcattttgcattttgcatttt
ttctatgagctcagtaagcaaggaaagaaggaaaggagatcttgcattttgcatttt
acctaagcgccccatcacacgtcatcttaatccaaacctcatgaattctctctct
ctctcatttttgagacagactctcgctctgtcaccaggctggatgcagtgccgt
ctcgactcattgcaacccgcctccggattcaatcaatttcattgccttagcactg
aggagctggattacaagtgacgcccaccatccggctaatcttgcatttttaga
gcaagatttgtcatgttgcctggatgttgcattttgcattttgcattttgcatttt
cacatcagccctccaaagtgtcattttgcattttgcattttgcattttgcatttt
tttttttttgcattttgcattttgcattttgcattttgcattttgcattttgcatttt
cagctcactgcaacccgcctccggattcaatgcattttgcattttgcattttgcatttt
tagctggactacaggctgcattttgcattttgcattttgcattttgcattttgcatttt
cagggatggatgcattttgcattttgcattttgcattttgcattttgcattttgcatttt
cctcaggctccaaagtgtgattacaggctgcattttgcattttgcattttgcatttt
ttctttctttttgcattttgcattttgcattttgcattttgcattttgcattttgcatttt
gaggctcactgcaacccgcctccggattcaatgcattttgcattttgcattttgcatttt
tcacaaggatgtggactacggcatgtgcattttgcattttgcattttgcatttt
aatatttttatattttatattttttttgcattttgcattttgcattttgcatttt
gcaatggatgtcatgttgcattttgcattttgcattttgcattttgcatttt
tcctgatgttgcattttgcattttgcattttgcattttgcattttgcatttt
tagtagagacaggatgttgcattttgcattttgcattttgcattttgcatttt
atccgcacccgcctcaggctccaaagtgtgattacaggatgtgacccgcaccac
cttattttatattttatattttatattttatattttatattttatattttatatttt
tgcccaggctggatgttgcattttgcattttgcattttgcattttgcatttt
caaggcttgcattttgcattttgcattttgcattttgcattttgcatttt
ccaggcttgcattttgcattttgcattttgcattttgcattttgcatttt
gtctcgactcctgacccgcctggatgttgcattttgcattttgcatttt
acaggcttgcattttgcattttgcattttgcattttgcattttgcatttt
tgtccaggctggatgttgcattttgcattttgcattttgcattttgcatttt
caagcgattctcctgtctcaggctccgcattttgcattttgcattttgcatttt
cccaggcttgcattttgcattttgcattttgcattttgcattttgcatttt
tcgaactcctgacccgcctggatgttgcattttgcattttgcatttt

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FIG. 3B

gtgtgagccactgcacctggccctgtatTTTgttagagatggggTTTcgccgtttgc
ccaggctggccccaaactccttaggttcaagcaattggctgcctggcctccaaagtgc
caggattacagggtgttaaggcattgcacccagccaagattaattttttgaagtacacaa
ctaggcaagtttagcaaaaccaagattaaacctaggcatccgagtcctgcctcaaacc
tgggtgtttaacactatactatactgtcctgcgttaggaacctatttagccaaatggca
gacttgaggctgagaaaagattcagaaggcctgccagtggagctaaacatTTgtgtgc
agccctgtctctgtataacttccggcttgccttattccaggctctgctgctgatga
agctgtgaccaaacgcacccaacccttggcagccatctgtcctgcagccatagcccaca
ttcccatgacccctctgtttggaccatgtctgtacagcctctaggccccagc
cccgagggtgaatgccatgcatgattctggtgtgctccatggcatccccagcctagctc
ccaatcccactttggcacg

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FIG. 4

ACACACATGCCATTGCGCTGTCCGTGCCGACTCCCCAACGCCTCTCGTTCTGGGAGGCCTT
 ACAGGGTGTACACACAAGAAGGTGGCTGGCACTTGGACCTTGGGTGGCAATTCCAGC
 TTAGCAACGCAGAAGAGTACAAAGTGTGGAAGGCAGGGCCCAGGGAAGGCAGTGCTGCTG
 GAAATGGCTTCTTAAACTGTGAGCACGCAGAGCACCCCTCTCCAGCGGTGGAAAGTGA
 TGCAGAGAGGCCACCGTCAGAGGGCAGAAGAGGACGAATGCCCTTGGGTGGCAGGG
 CATTAAACTGCTAAAAGCTGGTAGATGGAACAGAAAATGGCATTCTGGATCTAAACCG
 CCACAGGGCCTGAGAGCTGAAGAGCACCAGGTTGGACAAAGCTACTGAGATGCCT
 GTTCATCTGCTGACTTCTGTCTAGGCTATGGATGCCACCCCTTCATTCGGCCTAGG
 CTTCCCTGCTCACCACTGAGGCCTAATAACAAGAGTCTATGGACAGAACTACATTCTT
 TCTCGCATAGTGAATTGTGACAATTAGACTTGGCATCCAGCATGGGATAGTTGGGCAA
 GGCAAAACTAACTTAGAGTTCCCCCTCAACACATCCAAGTCAAACCCCTTTAGGTT
 ATCCTTCTCCATCACATCCCCTTTCCAGGCCTCCATTAGGTCTTAATATTCTT
 TTTCTTTCTCTCTCGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTT
 CTCTCTCTCCCTCTCTCTCTGTCCAGAGTAAGGATAAAATTCTTCTACTAAAGCAC
 TGGTTCTCAAACATTGGTCTCAGACCCACTCTAGAAATTGAGGATCTCAAAGAGCT
 TTGCTTATATTGGTCTTTGATACCTACACTAGAAATTAAAGCGAATACATT
 AAAATAATACACATGCACACATTACATTAGCCATGGGAGCAATAATGTCACCAACACA
 CTTCATGAAGCCTCTGGAAAACCTACAGTATACTTGTGAGAGAATGAGAGTGAAGGG
 CAAATAACATCTGTGTAGCAGTATTATGAAATTAGCTTGACCTCGTGGACTTCCTCAGAG
 GTTGGTCCCTGGATCACACTTGAGAACCATACTTGTCTGAAGTATTGGAGTTCATGT
 CTAACCTCTCCAGGGCATTATGTACAGTGTCTTTATTACTGTGGGGAGAGGGCAGTG
 CTAATAAAATTAACTACTGATAAAAAAAAAAAAAAG

FIG. 5

MLANSSTNS SVLPCPDYRP THRLHLVVYS LVLAAGLPLN ALALWVFLRA
 LRVHSVSVY MCNLAAASDLL FTLSLPVRLS YYALHHWPFP DLLCQTTGAI
FQMNMYGSCI FLMLINVDRY AAI VHPLRLR HLRRPRVARL LCLGVWALIL
VFAVPAARVH RPSRCRYRDL EVRLCFESFS DELWKGRLLP LVLLAEALGF
LLPLAAVVYS SGRVFWTLAR PDATQSQRRL KTVRLLLNL VIFLLCFVPY
NSTLAVYGLL RSKLVAASVP ARDRVRGVLM VMVLLAGANC VLDPLVYYFS
 AEGFRNTLRG LGTPHRARTS ATNGTRAALA QSERSAVTTD ATRPDAASQG
 LLRPSDSHSL SSFTQCPQDS AL

FIG. 6A

GP68_HUMAN
O46685
O15132
P2Y9_HUMAN
P2Y5_CHICK
P2Y5_HUMAN
HGPRBMY3
GPRH_HUMAN
O35811
SSR4_HUMAN

GP68_HUMAN
O46685
O15132
P2Y9_HUMAN
P2Y5_CHICK
P2Y5_HUMAN
HGPRBMY3
GPRH_HUMAN
O35811
SSR4_HUMAN

GP68_HUMAN
O46685
O15132
P2Y9_HUMAN
P2Y5_CHICK
P2Y5_HUMAN
HGPRBMY3
GPRH_HUMAN
O35811
SSR4_HUMAN

GP68_HUMAN
O46685
O15132
P2Y9_HUMAN
P2Y5_CHICK
P2Y5_HUMAN
HGPRBMY3
GPRH_HUMAN
O35811
SSR4_HUMAN

GP68_HUMAN
O46685
O15132
P2Y9_HUMAN
P2Y5_CHICK
P2Y5_HUMAN
HGPRBMY3
GPRH_HUMAN
O35811
SSR4_HUMAN

~~~~~MGNITADNSSMSCTIDHTIHQTLA  
~~~~~MGNITADNTSMNCIDHTIHQTLA  
~~~~~MGDRRFIDFQFQDSNSSLRPRLGNATANNTCIVD.DSFK..YNLN  
~~~~~MGDRRFIDFQFQDSNSSLRPRLGNATANNTCIVD.DSFK..YNLN  
~~~~~MVSSNCSTE.DSFK..YTLY  
~~~~~MVSVNSSHCFYN.DSFK..YTLY  
~~~~~MLANSSTNSSVLPCPDYPPTHRLH  
~~~~~MNGLEVAPPGLITNF..SLATAE.QCGQET.PLENMLF  
~~~~~MTSAESLLFTSICPSSSGDGDCRFNE.EFKFILL  
MSAPSTLPPGEEGLGTAWPSAANASSA~~A~~PAA~~E~~EAVAGPGDARAAGMVAI  
  
PVVVYTVLVWVGFPANCLSLYFGYLOIKARNELGVYLCLNLTVADLFYICSL  
PVVYV~~M~~VWVVGFPANCLSLYFGYLOIKARNELGVYLCLNLTVADLFYICSL  
GAVYSVVF~~T~~LGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTL  
GAVYSVVF~~T~~LGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTL  
GCVERSMVFV~~L~~G~~L~~IANCVAIYIETTFLKVRNETTTYMLNLAISDLLFVFTL  
GCMFSMFV~~L~~G~~L~~VSNCVAIYIETC~~V~~LKVRNETTTYMINLAMSDLLFVFTL  
LVVYSLVLAAGLPLNALALWVFLRAIRVHSVSVYMCNLAASDLLFTLSL  
ASFYLIIDFILALVGNTLALWLFI~~R~~DHKSGTPANVFLMHLAVADLSCVLVL  
PM~~S~~YAVV~~F~~V~~L~~GLALNAPTLWLB~~L~~FR~~I~~RPWDATATYMFHLALSDTLYV~~S~~L  
QC~~T~~YALVCLVGLVGNALV~~I~~FV~~I~~LYAKMKTATNTYELNLAVADELFMLSV  
  
PFWLQY.VLQHDNWSHGDLSCQVCGILLYENIYISVGFLCCISVD~~R~~Y~~L~~  
PFWLQY.VLQHDHWSHDD~~C~~QVCGILLYENIYISVGFLCCIS~~I~~D~~R~~Y~~L~~  
PF~~K~~IEYNF..NRHW~~P~~FGDTLCK~~K~~ISGTAF~~L~~NTIYGS~~M~~LFLTCISVDRE~~L~~  
PF~~K~~IEYNF..NRHW~~P~~FGDTLCK~~K~~ISGTAF~~L~~NTIYGS~~M~~LFLTCISVDRE~~L~~  
PFR~~I~~YYFV..VRNWPFGDV~~L~~CK~~K~~ISV~~T~~LFYTNMYGS~~I~~LFLTCISVDRE~~L~~  
PFR~~I~~YYFT..TRNWPFGD~~L~~CK~~K~~ISV~~M~~LFYTNMYGS~~I~~LFLTCISVDRE~~L~~  
PVRLSYYA..LHHWP~~E~~PD~~L~~COT~~T~~GATEQ~~M~~NYGS~~C~~FLML~~I~~NVD~~R~~YAAI  
PTELVYHFSG.NHW~~P~~FGETACRLTGFLFYLNMYAS~~I~~YFLTCISADRE~~L~~  
PT.LV~~Y~~YYAARNHW~~P~~FGT~~G~~LC~~K~~FRFLFY~~W~~LYCSV~~L~~FLTCISV~~H~~RYLG~~I~~  
PF..VASSAALRHWPFGS~~V~~LCRAVLS~~V~~DGLNM~~E~~TSV~~F~~CLTV~~L~~SVDRYV~~A~~  
  
AH~~P~~FRFHQFR~~T~~LKA~~A~~VGVS~~V~~WAKEL...LTSIYFLMHEEVIEDE~~N~~QHR  
AH~~P~~FRFHQFR~~T~~LKAAMGV~~S~~AL~~I~~W~~K~~E~~L~~...LTSIYFLMHEEVVEDADRHR  
VY~~P~~FRSR~~T~~TR~~T~~RRNSA~~I~~VCAGVW~~I~~VL~~S~~CG~~I~~SAS~~I~~FS..TTNV..NNATT  
VY~~P~~FRSR~~T~~TR~~T~~RRNSA~~I~~VCAGVW~~I~~VL~~S~~CG~~I~~SAS~~I~~FS..TTNV..NNATT  
VHPFRSK~~T~~LRTKR~~N~~ARI~~I~~VCVA~~W~~ITVLAG~~S~~TPAS~~F~~EQ..STNRONNTEQR  
V~~Y~~PEKSK~~T~~LRTKR~~N~~AKI~~I~~VC~~T~~GV~~W~~ITVIGGSAPA~~V~~FVQ..STHSQGNNA~~S~~E  
V~~H~~PLRLR~~H~~LR~~R~~PR~~V~~AR~~I~~CLGV~~W~~AL~~I~~LF~~V~~AMP~~A~~ARV~~H~~RPSRC~~R~~YDLEVR  
V~~H~~PV~~K~~SL~~K~~LR~~R~~PR~~F~~YAH~~I~~ACA~~I~~FL~~W~~.VVAVAMAP~~L~~VS~~P~~Q~~I~~V...OT~~N~~H~~T~~V  
CHPLRAIRWGR~~G~~PR~~F~~AS~~I~~LC~~G~~V~~W~~.VVAGC~~L~~VP~~N~~FF~~V~~T~~I~~...ANG~~T~~I  
V~~H~~PLRAATY~~R~~PSV~~A~~K~~I~~LN~~L~~GV~~W~~AS~~L~~LV~~T~~PI~~A~~..DTRPARGQAV  
  
VCFEH~~H~~YPIQAW~~R~~...A~~I~~NY~~Y~~REFLV~~G~~FL~~P~~IC~~L~~LLAS~~Y~~Q~~G~~I~~L~~RAV~~R~~RS~~H~~  
VCFEH~~H~~YPLE~~P~~R~~R~~...G~~I~~NY~~Y~~REFLV~~G~~FL~~P~~IC~~L~~LLAS~~Y~~RG~~I~~~~L~~RAV~~R~~RS~~H~~  
TC~~F~~EG~~L~~SKR~~W~~K~~T~~Y~~L~~SK~~I~~T~~I~~F~~I~~E~~V~~VG~~F~~II~~P~~L~~I~~LN~~V~~SC~~S~~SV~~L~~R~~T~~L~~R~~K~~P~~.A  
TC~~F~~EG~~E~~SKR~~W~~K~~T~~Y~~L~~SK~~I~~T~~I~~F~~I~~E~~V~~VG~~F~~II~~P~~L~~I~~LN~~V~~SC~~S~~SV~~L~~R~~T~~L~~R~~K~~P~~.A  
TC~~F~~EN~~E~~PE~~A~~TW~~K~~Y~~L~~SR~~I~~V~~I~~F~~I~~E~~V~~VG~~F~~II~~P~~L~~I~~LN~~V~~TC~~S~~TM~~V~~L~~R~~T~~L~~N~~K~~P.  
AC~~F~~EN~~E~~PE~~A~~TW~~K~~Y~~L~~SR~~I~~V~~I~~F~~I~~E~~V~~VG~~F~~II~~P~~L~~I~~LN~~V~~TC~~S~~SM~~V~~L~~K~~T~~L~~T~~K~~P.  
L~~C~~FE~~E~~SE~~S~~DELW~~K~~GR~~L~~LP~~V~~LLA~~E~~AL~~G~~FL~~L~~PL~~A~~AV~~V~~Y~~S~~GR~~V~~FW~~T~~L~~A~~RP~~D~~  
VC~~L~~O.LYREKASHHAL.M~~S~~AV~~V~~...AF~~T~~EP~~I~~TT~~V~~TC~~Y~~LL~~I~~IRS~~L~~RO~~G~~L.  
L~~C~~HD~~T~~LP~~E~~EFD~~H~~Y~~V~~.F~~S~~AV~~M~~V~~I~~L~~F~~GL~~P~~EL~~I~~IT~~L~~V~~C~~Y~~G~~LMARR~~L~~Y~~R~~PL~~P~~  
AC~~N~~LO~~W~~PH~~P~~AW~~S~~...AV~~V~~V~~V~~T~~F~~LL~~G~~FL~~L~~P~~V~~A~~I~~GL~~C~~Y~~L~~LV~~G~~K~~M~~RA~~V~~

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## FIG. 6B

GP68\_HUMAN  
O46685  
O15132  
P2Y9\_HUMAN  
P2Y5\_CHICK  
P2Y5\_HUMAN  
HGPRBMY3  
GPRH\_HUMAN  
O35811  
SSR4\_HUMAN

GP68\_HUMAN  
O46685  
O15132  
P2Y9\_HUMAN  
P2Y5\_CHICK  
P2Y5\_HUMAN  
HGPRBMY3  
GPRH\_HUMAN  
O35811  
SSR4\_HUMAN

GP68\_HUMAN  
O46685  
O15132  
P2Y9\_HUMAN  
P2Y5\_CHICK  
P2Y5\_HUMAN  
HGPRBMY3  
GPRH\_HUMAN  
O35811  
SSR4\_HUMAN

GP68\_HUMAN  
O46685  
O15132  
P2Y9\_HUMAN  
P2Y5\_CHICK  
P2Y5\_HUMAN  
HGPRBMY3  
GPRH\_HUMAN  
O35811  
SSR4\_HUMAN

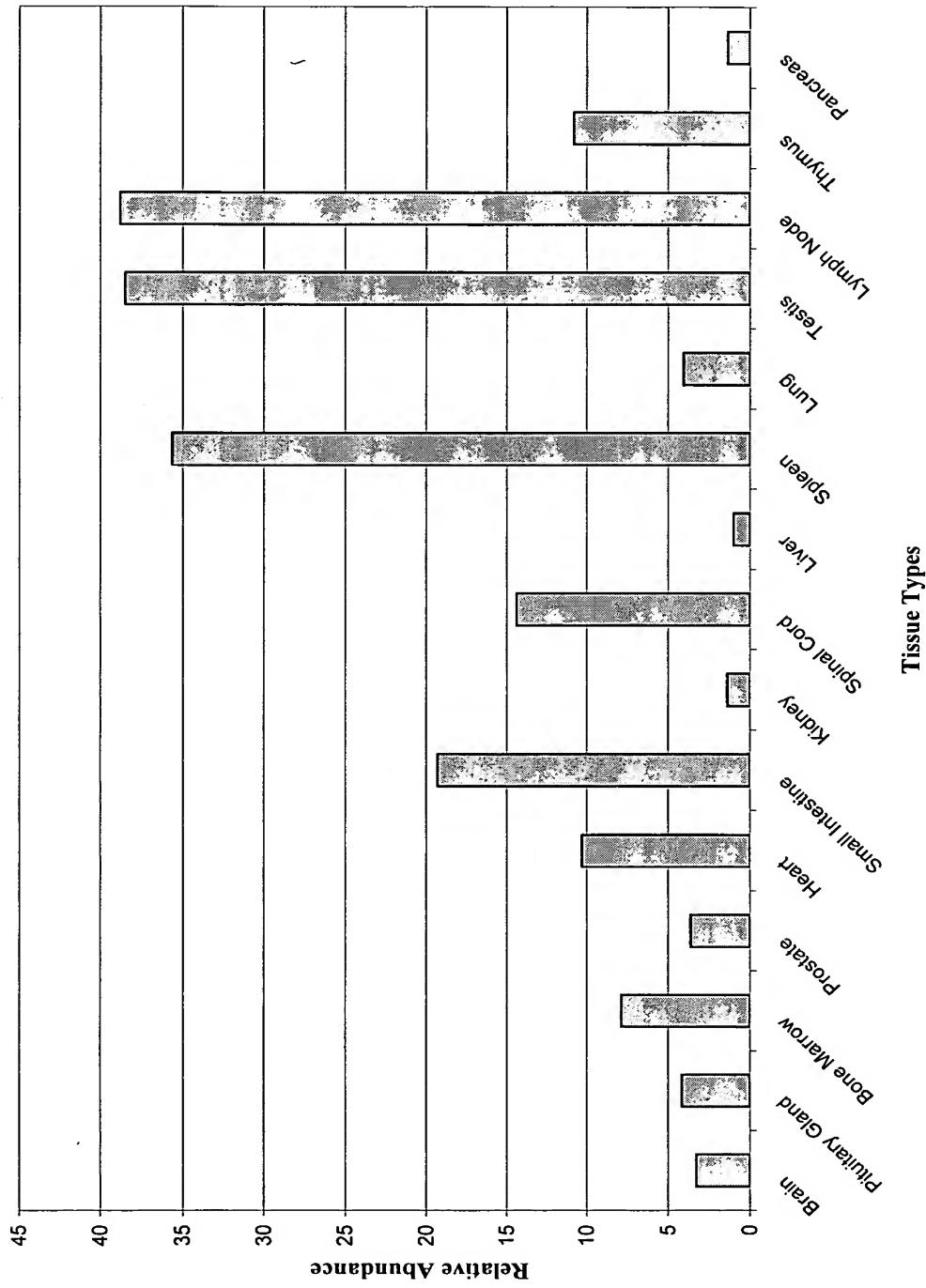
TQ.....KSRKDQTQRLVLSTVVIFLACFLPYHVIL....LVRSVWEASC  
TQ.....KSRKDQTQRLVLSTVVIFLACFLPYHVLL....LVRSLWESSC  
TLS..QIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAITNC  
TLS..QIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAITNC  
TLS..RNKLSKKKVLKMIKVHLVIFCFCFVVPYNITLILYSLMRTQTWINC  
TLS..RSKINKTKVLKMIKVHLIIFCFCFVVPYNINLILYSLVRTQTTFVNC  
TQS..Q...RRRKTVREILANLVIFLCFCFVVPYNSTLAVYGLRSKLVAAS  
.RV..EKRL.KTKAVRMIATVLAIFLVCFVPYHVNRSVYVLHYRSHGASC  
GAG..QSSS.RLRLSLRTIAVVLTVFAVCFVPEHTTRTIY.YQARLLQADC  
RAGWQORRRSEKKITREVLMVVVFLCWMPEYVYVQLNLVVTSDLAT..  
  
DFAKGVFN.AYHFSLLLTSFNCVADPVLYCFVSETTHDLARLRGACLAF  
DFAKGIFN.AYHFSLLLTSFNCVADPVLYCFVSETTHDLARLRGACLAF  
FEER.FAKIMYPITLCLATLNCCFDPFIYYFTLESFOKSFYI.NAHIRME  
FEER.FAKIMYPITLCLATLNCCFDPFIYYFTLESFOKSFYI.NAHIRME  
SMVT.AVRTMYPVTLCLIAVSNCDFDPIVYYFTSD..NSELDKKQQVHQN  
SMVA.AVRTMYPVTLCLIAVSNCDFDPIVYYFTSD..KMKKNWSVRRS  
VPARDRVRGVMVMLLAGANCVLDPLVYYFSAEGFRNTURGLGTPHRAR  
ATORI.LALANRITSCLTSNGALDPIMYFVAEKFRHALCNLLCGKRLK  
HVLNI.VNVVYKVTRPLASANSCLDPVBYLTGDKYRNOLQQLCRGSK..  
.....VNHVSLILSYANSCANPILYGLSDNFRSFQRVLC...LR  
  
LTCSRTGRAREAYPLGAPEASGKSGAQGEEPELITKLHPAFQTPNSPGSG  
LTCARTGRAREAYPLGAPEASGKS....EDPEVILTRLHPAFQTPHPPGMG  
SLFKTETPLTTKPSLPAIQEEVSDQTTNNNGEELMLESTF~~~~~  
SLFKTETPLTTKPSLPAIQEEVSDQTTNNNGEELMLESTF~~~~~  
T~~~~~  
DFRFSEVHGAENFIQHNLQTLKSKIFDNESAA~~~~~  
TSATNGTRAALAQSERSAVTTDATRPDAASQGLIRPSDSHSLSSFTQCPQ  
GPPPSFEGKTNESLSAKSEL~~~~~  
.PKP....RTAASSL.ALVTLHEESISRWADTHQDSTSFSAYEGDRL~~~  
CCLLEGAGGAEEEPLDYATALKS...KGGAGCMCPPLPCQQEALQPEPG

GFPTGRLA~~~~~  
GSPAGGLS~~~~~  
~~~~~  
~~~~~  
~~~~~  
~~~~~  
DSAL~~~~~  
~~~~~  
~~~~~  
RKRIPLTRTTF

| SEQUENCE   | SEQ ID NO: |
|------------|------------|
| GP68_HUMAN | 8          |
| O46685     | 9          |
| O15132     | 10         |
| P2Y9_HUMAN | 11         |
| P2Y5_CHICK | 12         |
| P2Y5_HUMAN | 13         |
| HGPRBMY3   | 2          |
| GPRH_HUMAN | 14         |
| O35811     | 15         |
| SSR4_HUMAN | 16         |

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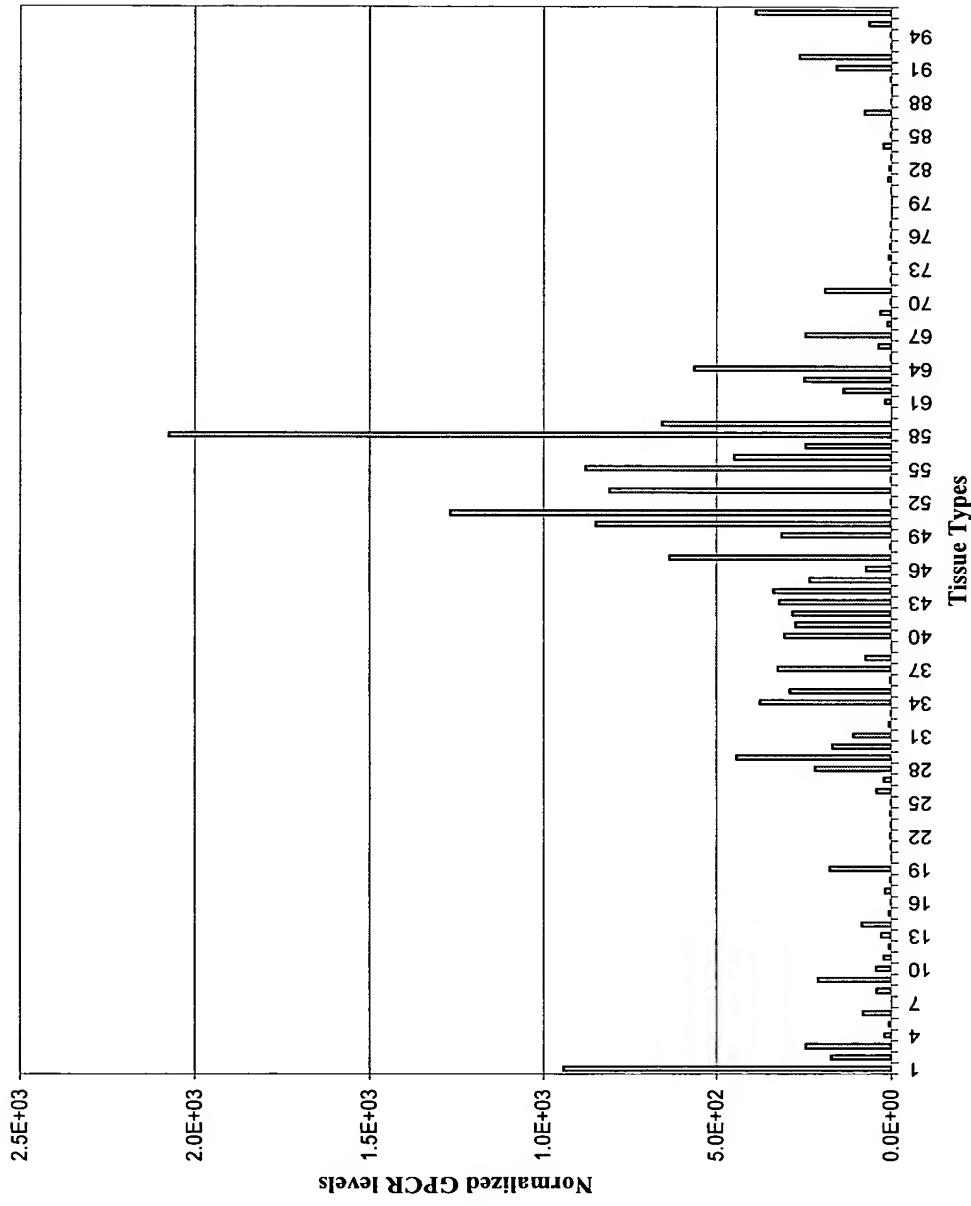
FIG. 7



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FIG. 8



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FIG. 9

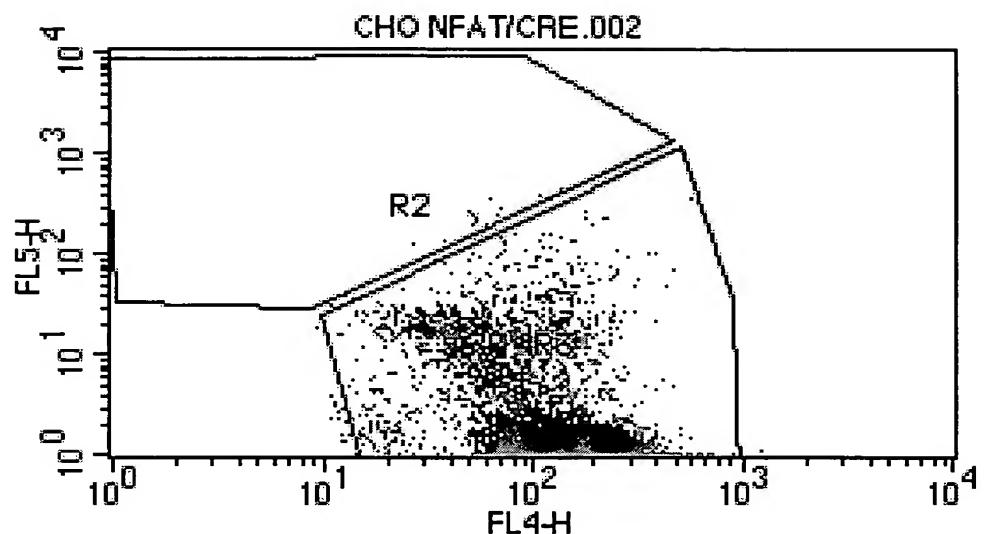
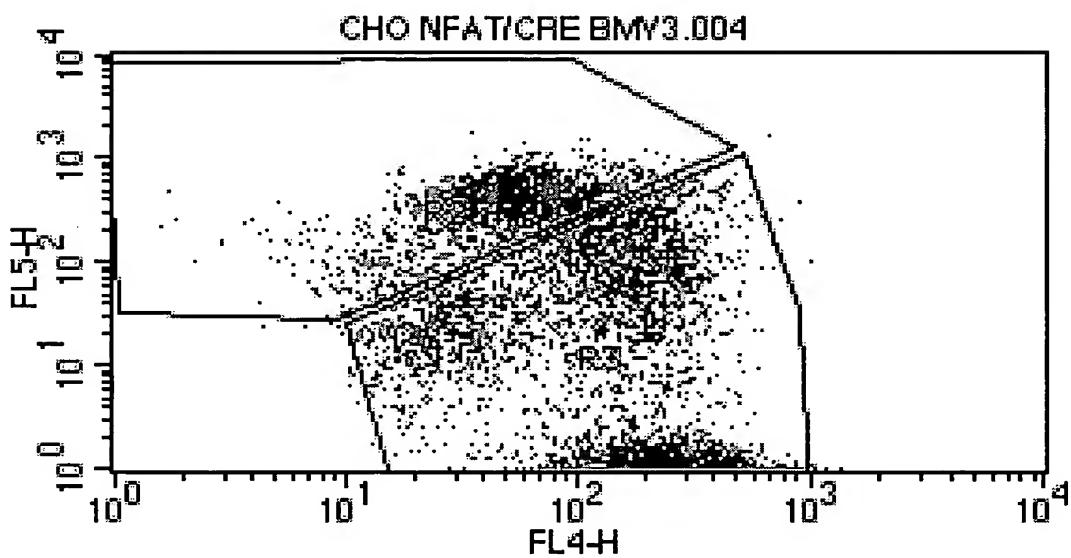


FIG. 10



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FIG. 11

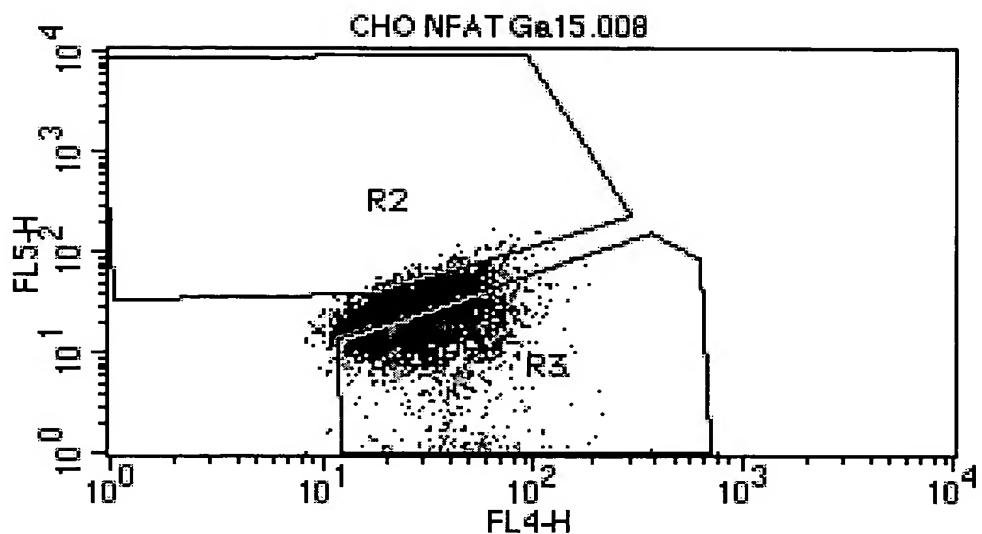
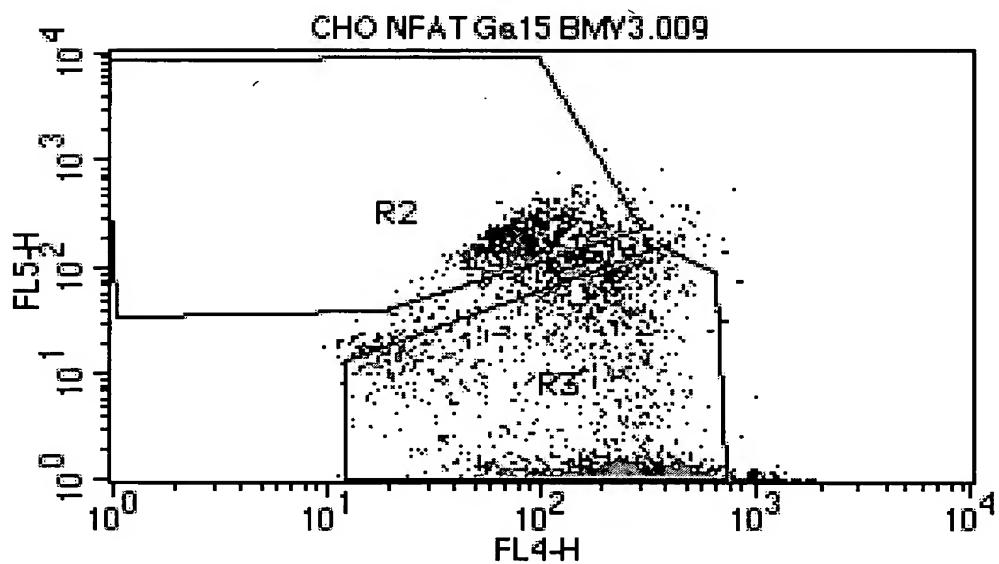
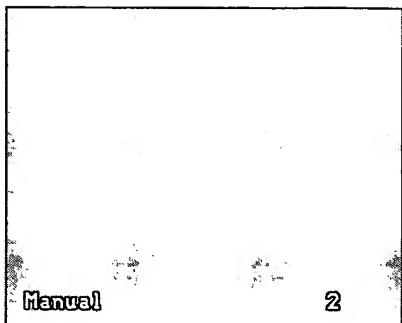


FIG. 12

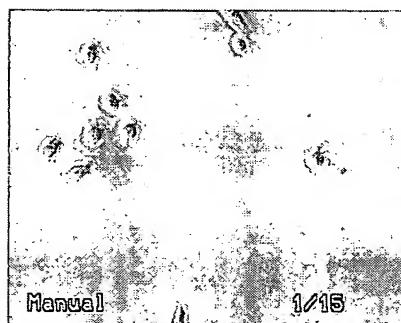


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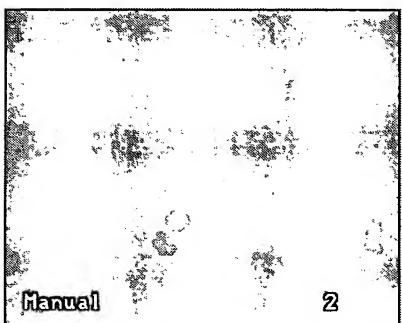
**FIG. 13A**



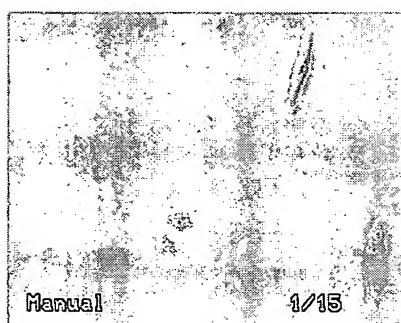
**FIG. 13B**



**FIG. 13C**

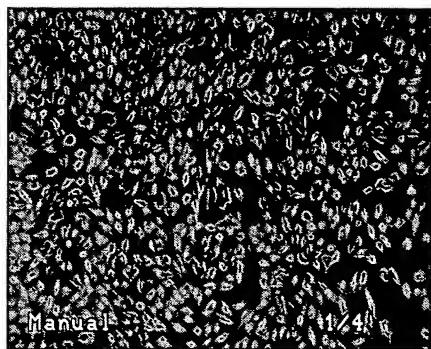


**FIG. 13D**

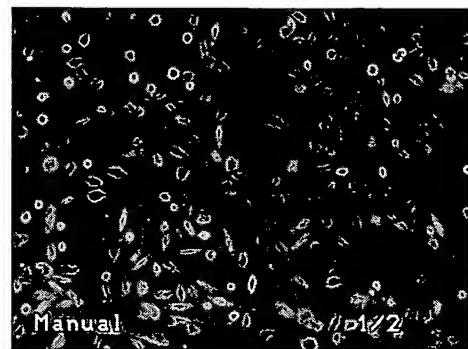


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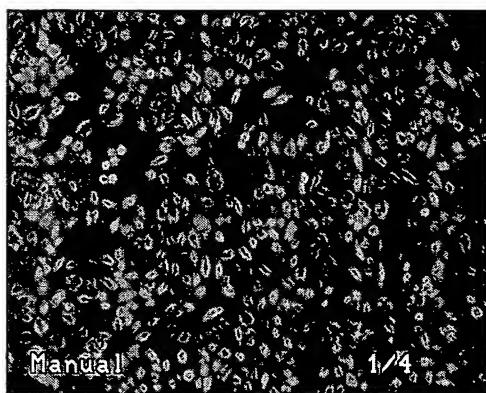
**FIG. 14A**



**FIG. 14B**



**FIG. 14C**



**FIG. 14D**

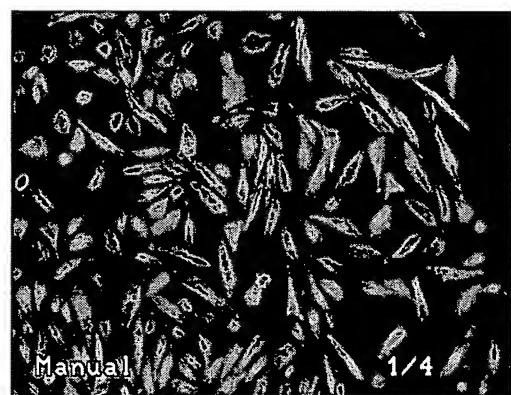
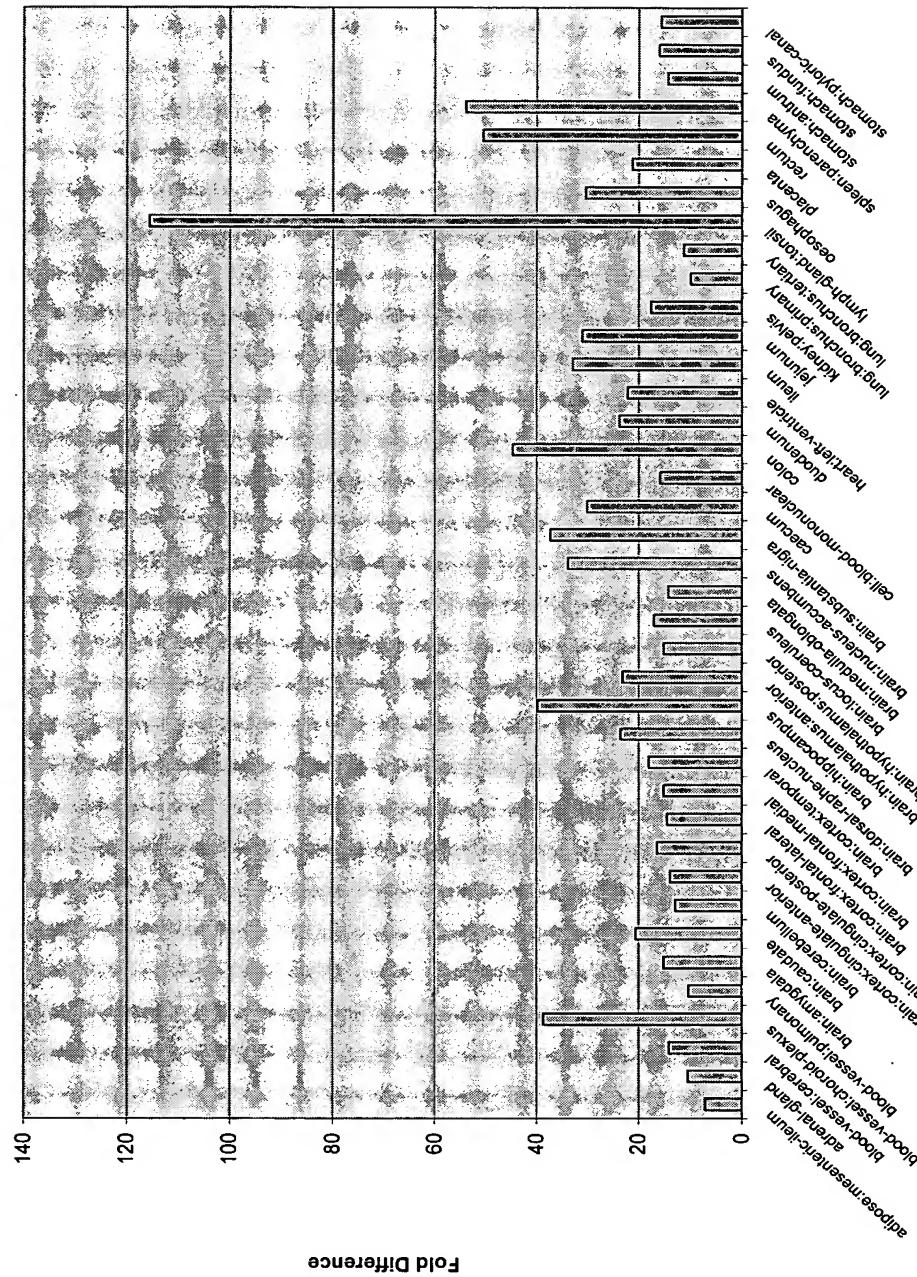
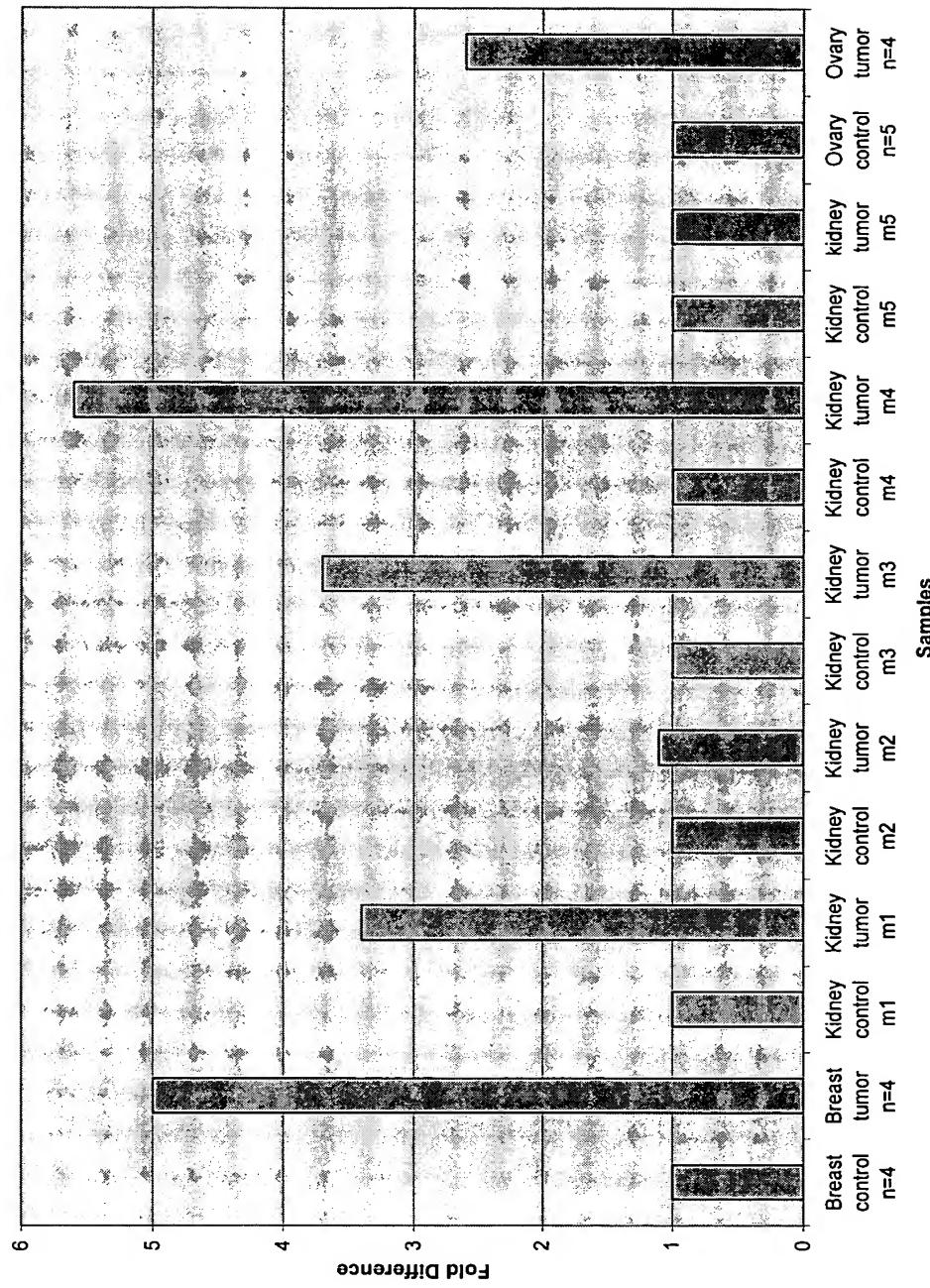


FIG. 15



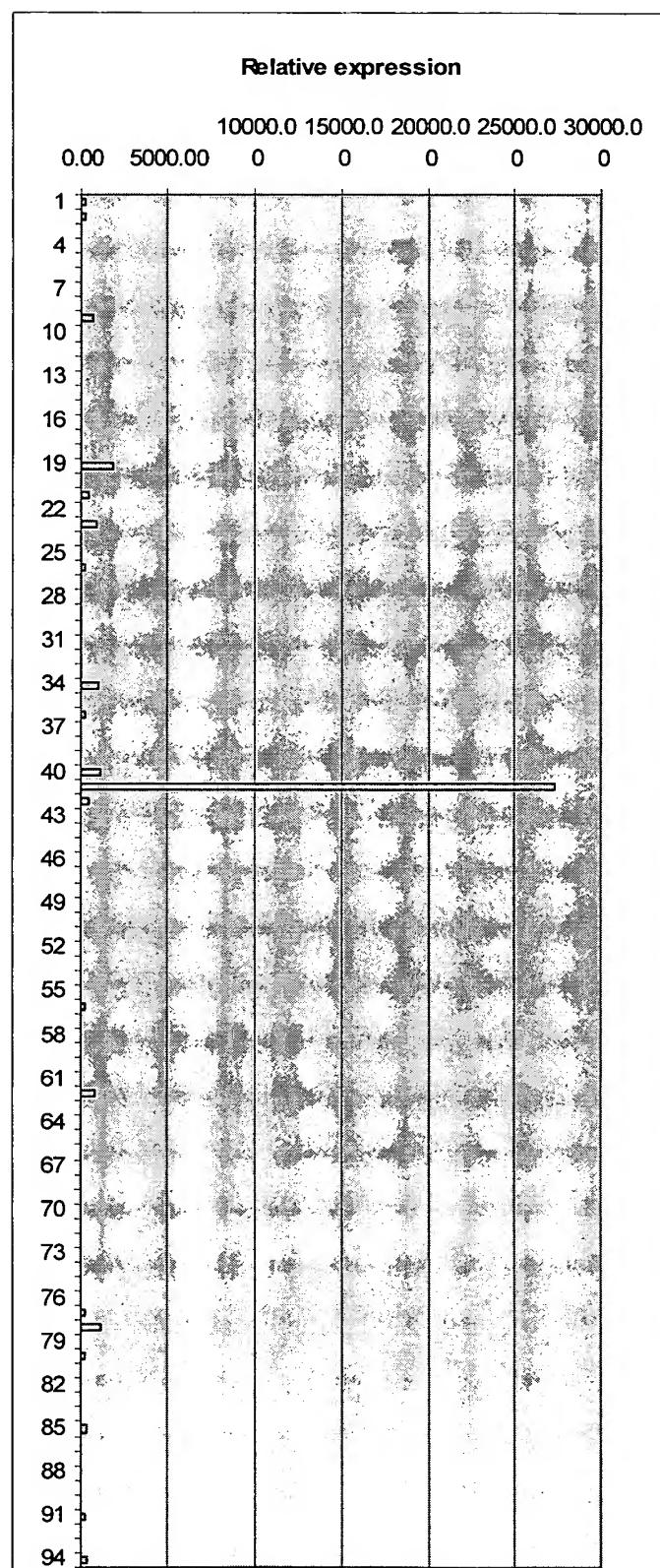
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FIG. 16



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FIG. 17



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**FIG. 18A**

| <u>BINDER NO.</u> | <u>SEQUENCE</u>  | <u>SEQ ID NO:</u> |
|-------------------|------------------|-------------------|
| 1                 | LEAKIWWVPAPS     | 17                |
| 2                 | TGQTKIWYPHST     | 18                |
| 3                 | VYSKVVLLPAGQ     | 19                |
| 4                 | HLKVWEVRSPGP     | 20                |
| 5                 | NAKVWTVPSKPP     | 21                |
| 6                 | KVWIPTSTWLQT     | 22                |
| 7                 | KVWSLDISAPQH     | 23                |
| 8                 | ADVLHATPSEKVWLL  | 24                |
| 9                 | KVVDMSNHKVWLVSQT | 25                |
| 10                | NHDNTKKVWILA     | 26                |
| 11                | KLWILADNFTNR     | 35                |
| 12                | INSPHELKKLWLPP   | 36                |
| 13                | FPHKLWVLVPVKT    | 37                |
| 14                | KLWTIPSNDYPP     | 38                |
| 15                | KLWELYPTVPAG     | 39                |
| 16                | KLWIPHTSQPFL     | 40                |
| 17                | KLWDITAPLPKP     | 41                |
| 18                | NAKLWQIPIAPH     | 42                |
| 19                | KLWVPQRPELV      | 43                |
| 20                | KLWELYPTVPAG     | 44                |
| 21                | TSTPHRVWQLPV     | 45                |
| 22                | TTPHRVWNLPLEAQO  | 46                |

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## FIG. 18B

| BINDER NO. | SEQUENCE                                                                                                                                                                                                   | SEQ ID NO:     |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|
| 1          | L E A K I W V V P A P S<br>TTG GAG GCG AAG ATT TGG GTG GTG CCT GCG CCT TCT<br>CTX GAO GCX AAO ATB TGG GTX CCX GCX CCX <u>TCX</u><br>TTO AGZ                                                                | 17<br>47<br>78 |
| 2          | T G Q T K I W Y P H S T<br>ACT GGG CAG ACT AAG ATT TGG TAT CCG CAT TCT ACG<br>GCX GGX CAO ACX AAO ATB TGG TAZ CCX CAZ <u>TCX</u> ACX<br>AGZ                                                                | 18<br>48<br>79 |
| 3          | V Y S K V W L L P A G Q<br>GTT TAT TCG AAG GTT TGG CTG CTT CCG GCG GGT CAG<br>GTX TAZ <u>TCX</u> AAO GTX TGG <u>CTX</u> <u>CTX</u> CCX GCX GGX CAO<br>AGZ CTO CTO                                          | 19<br>49<br>80 |
| 4          | H L K V W E V R S P G P<br>CAT CTT AAG GTG TGG GAG GTT CGG TCG CCT GGG CCT<br>CAZ <u>TCX</u> AAO GTX TGG GAO GTX <u>CGX</u> <u>TCX</u> CCX GGX CCX<br>TTO AGO AGZ                                          | 20<br>50<br>81 |
| 5          | N A K V W T V P S K P P<br>AAT GCG AAG GTG TGG ACG GTT CCG TCG AAG CCG CCT<br>AAZ GCX AAO GTX TGG ACX GTX CCX <u>TCX</u> AAO CCX CCX<br>AGZ                                                                | 21<br>51<br>82 |
| 6          | K V W I P T S T W L Q T<br>AAG GTG TGG ATT CCT ACG AGT ACT TGG CTG CAG ACT<br>AAO GTX TGG ATB CCX ACX <u>TCX</u> ACX TGG <u>CTX</u> CAO ACX<br>AGZ TTO                                                     | 22<br>52<br>83 |
| 7          | K V W S L D I S A P Q H<br>AAG GTT TGG AGT TTG GAT ATT TCG GCT CCG CAG CAT<br>AAO GTX TGG <u>TCX</u> <u>CTX</u> GAZ ATB <u>TCX</u> GCX CCX CAO CAZ<br>AGZ                                                  | 23<br>53<br>84 |
| 8          | A D V L H A T P S E K V W L L<br>GCG GAT GTG TTG CAT GCA TAC CCC TCT GAG AAG GTC TGG CTT CTG<br>GCX GAZ GTX <u>CTX</u> CAZ GCX ACX CCX <u>TCX</u> GAO AAO GTX TGG <u>CTX</u> <u>CTX</u><br>TTO AGZ TTO TTO | 24<br>54<br>85 |
| 9          | K V V D S N H K V W L V S Q T<br>AAG GTG GTG GAT AGT AAT CAT AAG GTT TGG CTG GTT TCT CAG ACT<br>AAO GTX GTX GAZ <u>TCX</u> AAZ CAZ AAO GTX TGG <u>CTX</u> GTX <u>TCX</u> CAO ACX<br>AGZ TTO AGZ            | 25<br>55<br>86 |
| 10         | N H D N T K K V W I L A<br>AAT CAT GAT AAT ACT AAG AAG GTT TGG ATT CTG GCT<br>AAZ CAZ GAZ AAZ ACX AAO AAO GTX TGG ATB <u>CTX</u> GCX<br>TTO                                                                | 26<br>56<br>87 |
| 11         | K L W I L A D N F T N R<br>AAG CTT TGG ATT CTG GCT GAT AAT TTT ACG AAT CGG<br>AAO <u>CTX</u> TGG ATB <u>CTX</u> GCX GAZ AAZ TTZ ACX AAZ <u>CGX</u><br>TTO TTO AGO                                          | 35<br>57<br>88 |

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## FIG. 18C

| BINDER NO. | SEQUENCE                                                                                                                                                                                                                                                  | SEQ ID NO:     |
|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|
| 12         | I N S P H E L K K L W L L P P<br>ATT AAT TCT CCG CAT GAA CTT AAG AAG CTG TGG CTT CTG CCT CCG CCT<br>ATB AAZ <u>TCX</u> CCX CAZ GAO <u>CTX</u> AAO AAO <u>CTX</u> TGG <u>CTX</u> CCT CCX CCX<br>AGX <u>TTO</u> <u>TTO</u> <u>TTO</u> <u>TTO</u> <u>TTO</u> | 36<br>57<br>89 |
| 13         | F P H K L W V L P V K T<br>TTT CCG CAT AAG TTG TGG GTT TTG CCG GTG AAG ACT<br>TTZ CCX CAZ AAO <u>CTX</u> TGG GTX <u>CTX</u> CCX GTX AAO ACX<br>TTO <u>TTO</u>                                                                                             | 37<br>58<br>90 |
| 14         | K L W T I P S N D Y P P<br>AAG CTG TGG ACG ATT CCT AGT AAT GAT TAT CCG CCT<br>AAO <u>CTX</u> TGG ACX ATB CCX <u>TCX</u> AAZ GAZ TAZ CCX CCX<br>TTO AGZ                                                                                                    | 38<br>59<br>91 |
| 15         | K L W E L Y P T V P A G<br>AAG CTT TGG GAG TTG TAT CCG ACT GTG CCG GCT GGT<br>AAO <u>CTX</u> TGG GAO <u>CTX</u> TAZ CCX ACX GTX CCX GCX GGX<br>TTO <u>TTO</u>                                                                                             | 39<br>60<br>92 |
| 16         | K L W I P H T S Q P F L<br>AAG CTG TGG ATT CCT CAT ACT TCT CAG CCG TTT CTT<br>AAO <u>CTX</u> TGG ATB CCX CAZ ACX <u>TCX</u> CAO CCX TTZ <u>CTX</u><br>TTO AGZ <u>TTO</u>                                                                                  | 40<br>61<br>93 |
| 17         | K L W D I T A P L P K P<br>AAG TTG TGG GAT ATT ACG GCT CCT TTG CCT AAG CCT<br>AAO <u>CTX</u> TGG GAZ ATB ACX GCX CCX <u>CTX</u> CCX AAO CCX<br>TTO                                                                                                        | 41<br>62<br>94 |
| 18         | N A K L W Q I P A I P H<br>AAT GCG AAG CTT TGG TAG ATT CCT GCG ATT CCG CAT<br>AAZ GCX AAO <u>CTX</u> TGG CAO ATB CCX GCX ATB CCX CAZ<br>TTO                                                                                                               | 42<br>63<br>95 |
| 19         | K L W V P Q N R P E L V<br>AAG CTT TGG GTT CCG CAG AAT CGT CCG GAG CTG GTG<br>AAO <u>CTX</u> TGG GTX CCX CAO AAO <u>CGX</u> CCX GAO <u>CTX</u> GTX<br>TTO AGO <u>TTO</u>                                                                                  | 43<br>67<br>96 |
| 20         | K L W E L Y P T V P A G<br>AAG CTT TGG GAG TTG TAT CCG ACT GTG CCG GCT GGT<br>AAO <u>CTX</u> TGG GAO <u>CTX</u> TAZ CCX ACX GTX CCX GCX GGX<br>TTO TTO                                                                                                    | 44<br>68<br>97 |
| 21         | T S T P H R V W Q L P V<br>ACT TCT ACT CCT CAT AGG GTT TGG CAG CTG CCT GTT<br>ACX <u>TCX</u> ACX CCX CAZ <u>CGX</u> GTX TGG CAO <u>CTX</u> CCX GTX<br>AGZ AGO <u>TTO</u>                                                                                  | 45<br>69<br>98 |
| 22         | T T P H R V W N L P L E A Q Q<br>ACT ACT CCT CAT CGT GTA TGG AAC CTG CCC CTG GAG GCT CAG CAG<br>ACX ACX CCX CAZ <u>CGX</u> GTX TGG AAO <u>CTX</u> CCX <u>CTX</u> GAO GCX CAO CAO<br>AGO <u>TTO</u> <u>TTO</u>                                             | 46<br>70<br>99 |

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**FIG. 19A**

| <u>GPC RECEPTOR</u> | <u>BINDER SEQUENCE</u> | <u>SEQ ID NO:</u> |
|---------------------|------------------------|-------------------|
| HGPRBMY11           | THGFGRVWSVPLRS         | 73                |
| HGPRBMY23           | SRVSGAKVWFLSNWS        | 74                |
| P2Y10               | AMNSHKIWLPH            | 75                |
| P2Y10               | GLKIWSLPPHHG           | 76                |
| P2Y10               | KVWQMAPTTAFS           | 77                |

**FIG. 19B**

| <u>GPC RECEPTOR</u> | <u>BINDER SEQUENCE</u>                                                                                                                                                                 | <u>SEQ ID NO:</u> |
|---------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|
| HGPRBMY11           | T H G F G H R V W S V P L R S<br>ACT CAT GGT TTT GGT CAT CGT GTG TGG AGT GTT CCG TTG CGT TCG<br>ACX CAZ GGX TTZ GGX CAZ CGX GTX TGG TCX GTX CCX CTX CGX TCX<br>AGO AGZ TTO AGO AGZ     | 73<br>100<br>105  |
| HGPRBMY23           | S R V S G A K V W F L S N W S<br>AGT AGG GTG TCT GGT GCG AAG GTT TGG TTT TTG AGT AAT TGG TCT<br>TCX CGX GTX TCX GGX GCX AAO GTX TGG TTZ CTX TCX AAZ TGG TCX<br>AGZ AGO AGZ TTO AGZ AGZ | 74<br>101<br>106  |
| P2Y10               | A M N S H K I W M L P H<br>GCT ATG AAT AGT CAT AAG ATT TGG ATG TTG CCG CAT<br>GCX ATG AAZ TCX CAZ AAO ATB TGG ATG CTX CCX CAZ<br>AGZ TTO                                               | 75<br>102<br>107  |
| P2Y10               | G L K I W S L P H H G<br>GGT CTG AAG ATT TGG AGT TTG CCG CCG CAT CAT GGG<br>GGX CTX AAO ATB TGG TCX CTX CCX CCX CAZ CAZ GGX<br>TTO AGZ TTO                                             | 76<br>103<br>108  |
| P2Y10               | K V W Q M A P T T A F S<br>AAG GTT TGG TAG ATG GCG CCT ACG ACT GCG TTT TCG<br>AAO GTX TGG CAO ATG GCX CCX ACX ACX GCX TTZ TCX<br>AGZ                                                   | 77<br>104<br>109  |

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**FIG. 20**

HGPRBMY11

MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL  
PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVT SIRSAWILCGIWI  
MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRV  
HRKALTTIITLIIIFFLCFLPYHTLRTVHLLTWKVGLCKDRLHKALVITLALAAAANC FNPLLYYFAGENFKDRL  
KSALRKGHPOKAKTKCVFPVS VWRKETRV (SEQ ID NO: 110)

HGPRBMY23

MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSSTIIMLN  
ACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCA  
VVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKWYNLILTATTFCLPLVIVTLCYTTIHTL  
THGLQTDCLKQKARRLTILLLAFYVCFLPFHILRVIRIESRLLSISCSIENQIHEAYIVSRPLAALNTFGNLL  
LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP (SEQ ID NO: 111)

P2Y10

MANLDKYTETFKMGNSTSTAEIFYCVENTNVKFQYSLYATTYILIFI PGLLANSAAALWVLCRFISKKNKAIIFMIN  
LSVADLAHVLSLPLRIYYYISHHWPFQRALCLLCFYLKYLKLNMYASICFLTCISLQRCFFLLKPFRARDWKRRYDV  
GISAAIWIVVGTACLPFPILRSTD LNNNKSCFADLGYKQMNAVALVGMITVAELAGFVI PVIIIAWCTWKTTISL  
RQPPMAFQG I SERQKALRMVFMC AAVFFICFTPYHINFIFYTMVKETIISSCP VV RIALYFHPFCLCLASLCCLL  
DPILYYFMASEFRDQLSRHGSSVTRSRLMSKESGSSMIG (SEQ ID NO: 112)